

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2007; month=12; day=6; hr=11; min=27; sec=41; ms=538;]

=====

Application No: 10759256 Version No: 2.0

Input Set:**Output Set:**

Started: 2007-11-16 19:19:16.385
Finished: 2007-11-16 19:19:18.648
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 263 ms
Total Warnings: 35
Total Errors: 0
No. of SeqIDs Defined: 35
Actual SeqID Count: 35

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-11-16 19:19:16.385
Finished: 2007-11-16 19:19:18.648
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 263 ms
Total Warnings: 35
Total Errors: 0
No. of SeqIDs Defined: 35
Actual SeqID Count: 35

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SUBSTITUTE SEQUENCE LISTING

<110> Conseiller, Emmanuel
 Debussche, Laurent
 Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 10759256

<141> 2004-01-20

<150> 09/829,936

<151> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide 5'-1 (p53)

<400> 1

agatctgtat ggaggagccg cag

23

<210> 2

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide 3' -393 (p53)

<400> 2

agatctcatc agtctgagtc aggcccttc

29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide H175 3'

<400> 3

ggggcagtg ctcac

15

<210> 4

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide W248 3'

<400> 4

gggcctccag ttcac

15

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide H273 3'

<400> 5

acaaacatgc acctc

15

<210> 6

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide G281 3'

<400> 6

gcgcgcgcct ctccc

15

<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide 5'-73

<400> 7

agatctgtgt ggcccctgca cca

23

<210> 8

<211> 1021

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 8

tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg gac	48
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp	
1 5 10 15	
ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg	96
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu	
20 25 30	
ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct	144
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro	
35 40 45	
aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca	192
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro	
50 55 60	
tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt	240
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys	
65 70 75 80	
aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc	288
Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile	
85 90 95	
gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac	336
Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn	
100 105 110	
gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg	384
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu	
115 120 125	
gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac	432
Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His	
130 135 140	
caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc	480
Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg	
145 150 155 160	
tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac	528
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp	
165 170 175	
aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct	576
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro	
180 185 190	
tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg	624
Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val	
195 200 205	
cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt gcc	672
Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala	
210 215 220	

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275 280 285

Phe Val Gly Ala Tyr Thr Phe

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide c-myc 5'

<400> 10

gatccatgga gcagaagctg atctccgagg aggacctga

39

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide c-myc 3'

<400> 11

gatctcaggt cctcctcgga gatcagcttc tgctccatg

39

<210> 12

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' MCS oligonucleotide

<400> 12

gatctcgggc gacctgcatg caattccggg gtgcggccgc gagct

45

<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' MCS oligonucleotide

<400> 13

cgcgggccgca cccgggaatt gcatgcaggt cgaccga

37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide 3' mMBP1

<400> 14

cgggtactggc agaggtaact gg

22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<220>

<221> CDS

<222> (49)..(1377)

<400> 15

gctgtggcag aaaccctga cttctgccca ccacctccca gcctcagg atg ctc cct
Met Leu Pro
1

57

ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg
Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu
5 10 15

105

ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser

153

20	25	30	35	
tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac				201
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His				
	40	45	50	
tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt				249
Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly				
	55	60	65	
gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc				297
Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg				
	70	75	80	
tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca				345
Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro				
	85	90	95	
gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct				393
Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro				
100	105	110	115	
gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg				441
Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu				
	120	125	130	
cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac				489
His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr				
	135	140	145	
cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg				537
Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val				
	150	155	160	
gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac				585
Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn				
	165	170	175	
ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga				633
Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly				
180	185	190	195	
cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc				681
Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala				
	200	205	210	
cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc				729
Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg				
	215	220	225	
tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat				777
Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp				
	230	235	240	
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc				825
Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val				
	245	250	255	

aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg	873
Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu	
260 265 270 275	
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca	921
Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala	
280 285 290	
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac	969
His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr	
295 300 305	
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca	1017
Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser	
310 315 320	
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag	1065
Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln	
325 330 335	
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt	1113
Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser	
340 345 350 355	
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt	1161
Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly	
360 365 370	
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc	1209
Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe	
375 380 385	
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg	1257
Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg	
390 395 400	
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc	1305
Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr	
405 410 415	
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg	1353
Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr	
420 425 430 435	
gtc ttt gtg gga gcc tat acc ttc tgaagaccct cagggaaggg ccatgtgggg	1407
Val Phe Val Gly Ala Tyr Thr Phe	
440	
gccccctccc cctcccatag ctttaagcagc cccggggggcc tagggatgac cgttctgctt	1467
aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa	1513

<210> 16

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

Met Leu Pro Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
1 5 10 15

Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pr